



# SEQUENCE LISTING

<110> Werner Seeger  
 <120> Novel Chimeric Plasminogen Activators and Their Pharmaceutical Use  
 <130> 607927-000001  
 <140> US/10/583,785  
 <141> 2006-06-19

<160> 26

<210> 1  
 <211> 1143  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) ... (1143)  
 <223> Coding sequence of the surfactant protein B precursor

<400> 1

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Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr	
1 5 10 15	
ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	
20 25 30	
gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag	144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	
35 40 45	
tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga	192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	
50 55 60	
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac	240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	
65 70 75 80	
aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg	288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	
85 90 95	
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc	336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	
100 105 110	
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag	384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	
115 120 125	
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa	432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	
130 135 140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg	480

Ser 145	Arg	Gln	Pro	Glu	Pro 150	Glu	Gln	Glu	Pro	Gly 155	Met	Ser	Asp	Pro	Leu 160	
ccc Pro	aaa Lys	cct Pro	ctg Leu	cgg Arg 165	gac Asp	cct Pro	ctg Leu	cca Pro	gac Asp 170	cct Pro	ctg Leu	ctg Leu	gac Asp	aag Lys 175	ctc Leu	528
gtc Val	ctc Leu	cct Pro	gtg Val 180	ctg Leu	ccc Pro	ggg Gly	gcc Ala	ctc Leu 185	cag Gln	gcg Ala	agg Arg	cct Pro	ggg Gly 190	cct Pro	cac His	576
aca Thr	cag Gln	gat Asp 195	ctc Leu	tcc Ser	gag Glu	cag Gln	caa Gln 200	ttc Phe	ccc Pro	att Ile	cct Pro	ctc Leu 205	ccc Pro	tat Tyr	tgc Cys	624
tgg Trp	ctc Leu 210	tgc Cys	agg Arg	gct Ala	ctg Leu	atc Ile 215	aag Lys	cgg Arg	atc Ile	caa Gln	gcc Ala 220	atg Met	att Ile	ccc Pro	aag Lys	672
ggt Gly 225	gcg Ala	cta Leu	gct Ala	gtg Val	gca Ala 230	gtg Val	gcc Ala	cag Gln	gtg Val	tgc Cys 235	cgc Arg	gtg Val	gta Val	cct Pro	ctg Leu 240	720
gtg Val	gcg Ala	ggc Gly	ggc Gly	atc Ile 245	tgc Cys	cag Gln	tgc Cys	ctg Leu	gct Ala 250	gag Glu	cgc Arg	tac Tyr	tcc Ser	gtc Val 255	atc Ile	768
ctg Leu	ctc Leu	gac Asp	acg Thr 260	ctg Leu	ctg Leu	ggc Gly	cgc Arg	atg Met 265	ctg Leu	ccc Pro	cag Gln	ctg Leu	gtc Val 270	tgc Cys	cgc Arg	816
ctc Leu	gtc Val	ctc Leu 275	cgg Arg	tgc Cys	tcc Ser	atg Met	gat Asp 280	gac Asp	agc Ser	gct Ala	ggc Gly	cca Pro 285	agg Arg	tcg Ser	ccg Pro	864
aca Thr	gga Gly 290	gaa Glu	tgg Trp	ctg Leu	ccg Pro	cga Arg 295	gac Asp	tct Ser	gag Glu	tgc Cys	cac His 300	ctc Leu	tgc Cys	atg Met	tcc Ser	912
gtg Val 305	acc Thr	acc Thr	cag Gln	gcc Ala	ggg Gly 310	aac Asn	agc Ser	agc Ser	gag Glu	cag Gln 315	gcc Ala	ata Ile	cca Pro	cag Gln	gca Ala 320	960
atg Met	ctc Leu	cag Gln	gcc Ala	tgt Cys 325	gtt Val	ggc Gly	tcc Ser	tgg Trp	ctg Leu 330	gac Asp	agg Arg	gaa Glu	aag Lys	tgc Cys 335	aag Lys	1008
caa Gln	ttt Phe	gtg Val	gag Glu 340	cag Gln	cac His	acg Thr	ccc Pro	cag Gln 345	ctg Leu	ctg Leu	acc Thr	ctg Leu	gtg Val 350	ccc Pro	agg Arg	1056
ggc Gly	tgg Trp	gat Asp 355	gcc Ala	cac His	acc Thr	acc Thr	tgc Cys 360	cag Gln	gcc Ala	ctc Leu	ggg Gly	gtg Val 365	tgt Cys	ggg Gly	acc Thr	1104
atg Met	tcc Ser 370	agc Ser	cct Pro	ctc Leu	cag Gln	tgt Cys 375	atc Ile	cac His	agc Ser	ccc Pro	gac Asp 380	ctt Leu				1143

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<212>      DNA
<213>      Homo sapiens

<220>
<221>      CDS
<222>      (1) ... (837)
<223>      Coding sequence of SP-B precursor lacking the C-terminal propeptide

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Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr
  1                    5                10                15

ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt      96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys
                    20                25                30

gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag      144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln
                    35                40                45

tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga      192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly
                    50                55                60

gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac      240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn
  65                    70                75                80

aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg      288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu
                    85                90                95

gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc      336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys
                    100               105               110

aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag      384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln
                    115               120               125

aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa      432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys
                    130               135               140

tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg      480
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu
 145                    150                155                160

ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc      528
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu
                    165                170                175

gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac      576
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His
                    180                185                190

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aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc	624
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tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag	672
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys	
210 215 220	
ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg	720
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu	
225 230 235 240	
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Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile	
245 250 255	
ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc	816
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg	
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Leu Val Leu Arg Cys Ser Met	
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<223> Coding sequence of the mature surfactant protein B	
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1 5 10 15	
cgg atc caa gcc atg att ccc aag ggt gcg cta gct gtg gca gtg gcc	96
Arg Ile Gln Ala Met Ile Pro Lys Gly Ala Leu Ala Val Ala Val Ala	
20 25 30	
cag gtg tgc cgc gtg gta cct ctg gtg gcg ggc ggc atc tgc cag tgc	144
Gln Val Cys Arg Val Val Pro Leu Val Ala Gly Gly Ile Cys Gln Cys	
35 40 45	
ctg gct gag cgc tac tcc gtc atc ctg ctc gac acg ctg ctg ggc cgc	192
Leu Ala Glu Arg Tyr Ser Val Ile Leu Leu Asp Thr Leu Leu Gly Arg	
50 55 60	
atg ctg ccc cag ctg gtc tgc cgc ctc gtc ctc cgg tgc tcc atg	237
Met Leu Pro Gln Leu Val Cys Arg Leu Val Leu Arg Cys Ser Met	
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<210> 4	
<211> 1293	

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<212>    DNA
<213>    Homo sapiens

<220>
<221>    CDS
<222>    (1) ... (1293)
<223>    Coding sequence of the single-chain urokinase-plasminogen activator

<400>    4

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Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser
  1          5          10          15

gac tcc aaa ggc agc aat gaa ctt cat caa gtt cca tcg aac tgt gac      96
Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
          20          25          30

tgt cta aat gga gga aca tgt gtg tcc aac aag tac ttc tcc aac att     144
Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
          35          40          45

cac tgg tgc aac tgc cca aag aaa ttc gga ggg cag cac tgt gaa ata     192
His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
          50          55          60

gat aag tca aaa acc tgc tat gag ggg aat ggt cac ttt tac cga gga     240
Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
  65          70          75          80

aag gcc agc act gac acc atg ggc cgg ccc tgc ctg ccc tgg aac tct     288
Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
          85          90          95

gcc act gtc ctt cag caa acg tac cat gcc cac aga tct gat gct ctt     336
Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
          100          105          110

cag ctg ggc ctg ggg aaa cat aat tac tgc agg aac cca gac aac cgg     384
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg
          115          120          125

agg cga ccc tgg tgc tat gtg cag gtg ggc cta aag ccg ctt gtc caa     432
Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln
          130          135          140

gag tgc atg gtg cat gac tgc gca gat gga aaa aag ccc tcc tct cct     480
Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro
          145          150          155          160

cca gaa gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc     528
Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg
          165          170          175

ttt aag att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg     576
Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp
          180          185          190

ttt gcg gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg     624
Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val

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195				200				205								
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tgc Cys 225	ttc Phe	att Ile	gat Asp	tac Tyr	cca Pro 230	aag Lys	aag Lys	gag Glu	gac Asp	tac Tyr 235	atc Ile	gtc Val	tac Tyr	ctg Leu	ggt Gly 240	720
cgc Arg	tca Ser	agg Arg	ctt Leu	aac Asn 245	tcc Ser	aac Asn	acg Thr	caa Gln	ggg Gly 250	gag Glu	atg Met	aag Lys	ttt Phe	gag Glu 255	gtg Val	768
gaa Glu	aac Asn	ctc Leu	atc Ile 260	cta Leu	cac His	aag Lys	gac Asp	tac Tyr 265	agc Ser	gct Ala	gac Asp	acg Thr	ctt Leu 270	gct Ala	cac His	816
cac His	aac Asn	gac Asp 275	att Ile	gcc Ala	ttg Leu	ctg Leu	aag Lys 280	atc Ile	cgt Arg	tcc Ser	aag Lys	gag Glu 285	ggc Gly	agg Arg	tgt Cys	864
gcg Ala	cag Gln 290	cca Pro	tcc Ser	cgg Arg	act Thr	ata Ile 295	cag Gln	acc Thr	atc Ile	tgc Cys	ctg Leu 300	ccc Pro	tcg Ser	atg Met	tat Tyr	912
aac Asn 305	gat Asp	ccc Pro	cag Gln	ttt Phe	ggc Gly 310	aca Thr	agc Ser	tgt Cys	gag Glu	atc Ile 315	act Thr	ggc Gly	ttt Phe	gga Gly	aaa Lys 320	960
gag Glu	aat Asn	tct Ser	acc Thr	gac Asp 325	tat Tyr	ctc Leu	tat Tyr	ccg Pro	gag Glu 330	cag Gln	ctg Leu	aaa Lys	atg Met	act Thr 335	gtt Val	1008
gtg Val	aag Lys	ctg Leu	att Ile 340	tcc Ser	cac His	cgg Arg	gag Glu	tgt Cys 345	cag Gln	cag Gln	ccc Pro	cac His	tac Tyr 350	tac Tyr	ggc Gly	1056
tct Ser	gaa Glu	gtc Val 355	acc Thr	acc Thr	aaa Lys	atg Met	ctg Leu 360	tgt Cys	gct Ala	gct Ala	gac Asp	cca Pro 365	cag Gln	tgg Trp	aaa Lys	1104
aca Thr	gat Asp 370	tcc Ser	tgc Cys	cag Gln	gga Gly	gac Asp 375	tca Ser	ggg Gly	gga Gly	ccc Pro	ctc Leu 380	gtc Val	tgt Cys	tcc Ser	ctc Leu	1152
caa Gln 385	ggc Gly	cgc Arg	atg Met	act Thr	ttg Leu 390	act Thr	gga Gly	att Ile	gtg Val	agc Ser 395	tgg Trp	ggc Gly	cgt Arg	gga Gly	tgt Cys 400	1200
gcc Ala	ctg Leu	aag Lys	gac Asp	aag Lys 405	cca Pro	ggc Gly	gtc Val	tac Tyr	acg Thr 410	aga Arg	gtc Val	tca Ser	cac His	ttc Phe 415	tta Leu	1248
ccc Pro	tgg Trp	atc Ile	cgc Arg 420	agt Ser	cac His	acc Thr	aag Lys	gaa Glu 425	gag Gln	aat Asn	ggc Gly	ctg Leu	gcc Ala 430	ctc Leu		1293

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 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
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 <222> (1) ... (828)  
 <223> Coding sequence of low mw two-chain urokinase-plasminogen activator  
  
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1 5 10 15	
act ctg agg ccc cgc ttt aag att att ggg gga gaa ttc acc acc atc	96
Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile	
20 25 30	
gag aac cag ccc tgg ttt gcg gcc atc tac agg agg cac cgg ggg ggc	144
Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly	
35 40 45	
tct gtc acc tac gtg tgt gga ggc agc ctc atc agc cct tgc tgg gtg	192
Ser Val Thr Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val	
50 55 60	
atc agc gcc aca cac tgc ttc att gat tac cca aag aag gag gac tac	240
Ile Ser Ala Thr His Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr	
65 70 75 80	
atc gtc tac ctg ggt cgc tca agg ctt aac tcc aac acg caa ggg gag	288
Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu	
85 90 95	
atg aag ttt gag gtg gaa aac ctc atc cta cac aag gac tac agc gct	336
Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala	
100 105 110	
gac acg ctt gct cac cac aac gac att gcc ttg ctg aag atc cgt tcc	384
Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser	
115 120 125	
aag gag ggc agg tgt gcg cag cca tcc cgg act ata cag acc atc tgc	432
Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys	
130 135 140	
ctg ccc tcg atg tat aac gat ccc cag ttt ggc aca agc tgt gag atc	480
Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile	
145 150 155 160	
act ggc ttt gga aaa gag aat tct acc gac tat ctc tat ccg gag cag	528
Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln	
165 170 175	
ctg aaa atg act gtt gtg aag ctg att tcc cac cgg gag tgt cag cag	576
Leu Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln	
180 185 190	

ccc	cac	tac	tac	ggc	tct	gaa	gtc	acc	acc	aaa	atg	ctg	tgt	gct	gct	624
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Asp	Pro	Gln	Trp	Lys	Thr	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	
	210					215					220					
ctc	gtc	tgt	tcc	ctc	caa	ggc	cgc	atg	act	ttg	act	gga	att	gtg	agc	720
Leu	Val	Cys	Ser	Leu	Gln	Gly	Arg	Met	Thr	Leu	Thr	Gly	Ile	Val	Ser	
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tgg	ggc	cgt	gga	tgt	gcc	ctg	aag	gac	aag	cca	ggc	gtc	tac	acg	aga	768
Trp	Gly	Arg	Gly	Cys	Ala	Leu	Lys	Asp	Lys	Pro	Gly	Val	Tyr	Thr	Arg	
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gtc	tca	cac	ttc	tta	ccc	tgg	atc	cgc	agt	cac	acc	aag	gaa	gag	aat	816
Val	Ser	His	Phe	Leu	Pro	Trp	Ile	Arg	Ser	His	Thr	Lys	Glu	Gln	Asn	
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<210> 6  
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<220>  
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 <222> (1) ... (837)  
 <223> Coding sequence of human SP-B precursor lacking the C-terminal propeptide

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 <222> (844) ... (1671)  
 <223> Coding sequence of low mw two-chain urokinase-plasminogen activator

<400> 6

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Met	Ala	Glu	Ser	His	Leu	Leu	Gln	Trp	Leu	Leu	Leu	Leu	Leu	Pro	Thr	
1				5				10						15		
ctc	tgt	ggc	cca	ggc	act	gct	gcc	tgg	acc	acc	tca	tcc	ttg	gcc	tgt	96
Leu	Cys	Gly	Pro	Gly	Thr	Ala	Ala	Trp	Thr	Thr	Ser	Ser	Leu	Ala	Cys	
			20					25					30			
gcc	cag	ggc	cct	gag	ttc	tgg	tgc	caa	agc	ctg	gag	caa	gca	ttg	cag	144
Ala	Gln	Gly	Pro	Glu	Phe	Trp	Cys	Gln	Ser	Leu	Glu	Gln	Ala	Leu	Gln	
		35					40					45				
tgc	aga	gcc	cta	ggg	cat	tgc	cta	cag	gaa	gtc	tgg	gga	cat	gtg	gga	192
Cys	Arg	Ala	Leu	Gly	His	Cys	Leu	Gln	Glu	Val	Trp	Gly	His	Val	Gly	
	50					55					60					

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aag Lys	atg Met	gcc Ala	aag Lys	gag Glu 85	gcc Ala	att Ile	ttc Phe	cag Gln	gac Asp 90	acg Thr	atg Met	agg Arg	aag Lys	ttc Phe 95	ctg Leu	288
gag Glu	cag Gln	gag Glu	tgc Cys 100	aac Asn	gtc Val	ctc Leu	ccc Pro	ttg Leu 105	aag Lys	ctg Leu	ctc Leu	atg Met	ccc Pro 110	cag Gln	tgc Cys	336
aac Asn	caa Gln	gtg Val 115	ctt Leu	gac Asp	gac Asp	tac Tyr	ttc Phe 120	ccc Pro	ctg Leu	gtc Val	atc Ile	gac Asp 125	tac Tyr	ttc Phe	cag Gln	384
aac Asn	cag Gln 130	act Thr	gac Asp	tca Ser	aac Asn	ggc Gly 135	atc Ile	tgt Cys	atg Met	cac His	ctg Leu 140	ggc Gly	ctg Leu	tgc Cys	aaa Lys	432
tcc Ser 145	cgg Arg	cag Gln	cca Pro	gag Glu	cca Pro 150	gag Glu	cag Gln	gag Glu	cca Pro	ggg Gly 155	atg Met	tca Ser	gac Asp	ccc Pro	ctg Leu 160	480
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aca Thr	cag Gln	gat Asp 195	ctc Leu	tcc Ser	gag Glu	cag Gln	caa Gln 200	ttc Phe	ccc Pro	att Ile	cct Pro	ctc Leu 205	ccc Pro	tat Tyr	tgc Cys	624
tgg Trp 210	ctc Leu	tgc Cys	agg Arg	gct Ala	ctg Leu	atc Ile 215	aag Lys	cgg Arg	atc Ile	caa Gln	gcc Ala 220	atg Met	att Ile	ccc Pro	aag Lys	672
ggc Gly 225	gcg Ala	cta Leu	gct Ala	gtg Val	gca Ala 230	gtg Val	gcc Ala	cag Gln	gtg Val	tgc Cys 235	cgc Arg	gtg Val	gta Val	cct Pro	ctg Leu 240	720
gtg Val	gcg Ala	ggc Gly	ggc Gly	atc Ile 245	tgc Cys	cag Gln	tgc Cys	ctg Leu	gct Ala 250	gag Glu	cgc Arg	tac Tyr	tcc Ser	gtc Val 255	atc Ile	768
ctg Leu	ctc Leu	gac Asp	acg Thr 260	ctg Leu	ctg Leu	ggc Gly	cgc Arg	atg Met 265	ctg Leu	ccc Pro	cag Gln	ctg Leu	gtc Val 270	tgc Cys	cgc Arg	816
ctc Leu	gtc Val	ctc Leu 275	cgg Arg	tgc Cys	tcc Ser	atg Met	aag Lys 280	ctt Leu	aag Lys	ccc Pro	tcc Ser	tct Ser 285	cct Pro	cca Pro	gaa Glu	864
gaa Glu 290	tta Leu	aaa Lys	ttt Phe	cag Gln	tgt Cys	ggc Gly 295	caa Gln	aag Lys	act Thr	ctg Leu	agg Arg 300	ccc Pro	cgc Arg	ttt Phe	aag Lys	912

att Ile 305	att Ile	ggg Gly	gga Gly	gaa Glu	ttc Phe 310	acc Thr	acc Thr	atc Ile	gag Glu	aac Asn 315	cag Gln	ccc Pro	tgg Trp	ttt Phe	gcg Ala 320	960
gcc Ala	atc Ile	tac Tyr	agg Arg	agg Arg 325	cac His	cgg Arg	ggg Gly	ggc Gly	tct Ser 330	gtc Val	acc Thr	tac Tyr	gtg Val	tgt Cys 335	gga Gly	1008
ggc Gly	agc Ser	ctc Leu	atc Ile 340	agc Ser	cct Pro	tgc Cys	tgg Trp	gtg Val 345	atc Ile	agc Ser	gcc Ala	aca Thr	cac His 350	tgc Cys	ttc Phe	1056
att Ile	gat Asp	tac Tyr 355	cca Pro	aag Lys	aag Lys	gag Glu	gac Asp 360	tac Tyr	atc Ile	gtc Val	tac Tyr	ctg Leu 365	ggc Gly	cgc Arg	tca Ser	1104
agg Arg	ctt Leu 370	aac Asn	tcc Ser	aac Asn	acg Thr	caa Gln 375	ggg Gly	gag Glu	atg Met	aag Lys	ttt Phe 380	gag Glu	gtg Val	gaa Glu	aac Asn	1152
ctc Leu 385	atc Ile	cta Leu	cac His	aag Lys	gac Asp 390	tac Tyr	agc Ser	gct Ala	gac Asp	acg Thr 395	ctt Leu	gct Ala	cac His	cac His	aac Asn 400	1200
gac Asp	att Ile	gcc Ala	ttg Leu	ctg Leu 405	aag Lys	atc Ile	cgt Arg	tcc Ser	aag Lys 410	gag Glu	ggc Gly	agg Arg	tgt Cys	gcg Ala 415	cag Gln	1248
cca Pro	tcc Ser	cgg Arg	act Thr 420	ata Ile	cag Gln	acc Thr	atc Ile	tgc Cys 425	ctg Leu	ccc Pro	tcg Ser	atg Met	tat Tyr 430	aac Asn	gat Asp	1296
ccc Pro	cag Gln	ttt Phe 435	ggc Gly	aca Thr	agc Ser	tgt Cys	gag Glu 440	atc Ile	act Thr	ggc Gly	ttt Phe	gga Gly 445	aaa Lys	gag Glu	aat Asn	1344
tct Ser	acc Thr 450	gac Asp	tat Tyr	ctc Leu	tat Tyr	ccg Pro 455	gag Glu	cag Gln	ctg Leu	aaa Lys	atg Met 460	act Thr	gtt Val	gtg Val	aag Lys	1392
ctg Leu 465	att Ile	tcc Ser	cac His	cgg Arg	gag Glu 470	tgt Cys	cag Gln	cag Gln	ccc Pro	cac His 475	tac Tyr	tac Tyr	ggc Gly	tct Ser	gaa Glu 480	1440
gtc Val	acc Thr	acc Thr	aaa Lys	atg Met 485	ctg Leu	tgt Cys	gct Ala	gct Ala	gac Asp 490	cca Pro	cag Gln	tgg Trp	aaa Lys	aca Thr 495	gat Asp	1488
tcc Ser	tgc Cys	cag Gln	gga Gly 500	gac Asp	tca Ser	ggg Gly	gga Gly	ccc Pro 505	ctc Leu	gtc Val	tgt Cys	tcc Ser	ctc Leu 510	caa Gln	ggc Gly	1536
cgc Arg	atg Met	act Thr 515	ttg Leu	act Thr	gga Gly	att Ile	gtg Val 520	agc Ser	tgg Trp	ggc Gly	cgt Arg	gga Gly 525	tgt Cys	gcc Ala	ctg Leu	1584
aag Lys	gac Asp 530	aag Lys	cca Pro	ggc Gly	gtc Val	tac Tyr 535	acg Thr	aga Arg	gtc Val	tca Ser	cac His 540	ttc Phe	tta Leu	ccc Pro	tgg Trp	1632

atc	cgc	agt	cac	acc	aag	gaa	gag	aat	ggc	ctg	gcc	ctc					1671
Ile	Arg	Ser	His	Thr	Lys	Glu	Gln	Asn	Gly	Leu	Ala	Leu					
545					550					555							

<210> 7  
 <211> 1674  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1) ... (837)  
 <223> Coding sequence of human SP-B precursor lacking the C-terminal propeptide

<220>  
 <221> CDS  
 <222> (847) ... (1674)  
 <223> Coding sequence of low mw two-chain urokinase-plasminogen activator

<400> 7

atg	gct	gag	tca	cac	ctg	ctg	cag	tgg	ctg	ctg	ctg	ctg	ctg	ccc	acg		48
Met	Ala	Glu	Ser	His	Leu	Leu	Gln	Trp	Leu	Leu	Leu	Leu	Leu	Pro	Thr		
1				5					10					15			
ctc	tgt	ggc	cca	ggc	act	gct	gcc	tgg	acc	acc	tca	tcc	ttg	gcc	tgt		96
Leu	Cys	Gly	Pro	Gly	Thr	Ala	Ala	Trp	Thr	Thr	Ser	Ser	Leu	Ala	Cys		
			20					25					30				
gcc	cag	ggc	cct	gag	ttc	tgg	tgc	caa	agc	ctg	gag	caa	gca	ttg	cag		144
Ala	Gln	Gly	Pro	Glu	Phe	Trp	Cys	Gln	Ser	Leu	Glu	Gln	Ala	Leu	Gln		
		35					40					45					
tgc	aga	gcc	cta	ggg	cat	tgc	cta	cag	gaa	gtc	tgg	gga	cat	gtg	gga		192
Cys	Arg	Ala	Leu	Gly	His	Cys	Leu	Gln	Glu	Val	Trp	Gly	His	Val	Gly		
	50					55					60						
gcc	gat	gac	cta	tgc	caa	gag	tgt	gag	gac	atc	gtc	cac	atc	ctt	aac		240
Ala	Asp	Asp	Leu	Cys	Gln	Glu	Cys	Glu	Asp	Ile	Val	His	Ile	Leu	Asn		
	65				70					75					80		
aag	atg	gcc	aag	gag	gcc	att	ttc	cag	gac	acg	atg	agg	aag	ttc	ctg		288
Lys	Met	Ala	Lys	Glu	Ala	Ile	Phe	Gln	Asp	Thr	Met	Arg	Lys	Phe	Leu		
				85					90					95			
gag	cag	gag	tgc	aac	gtc	ctc	ccc	ttg	aag	ctg	ctc	atg	ccc	cag	tgc		336
Glu	Gln	Glu	Cys	Asn	Val	Leu	Pro	Leu	Lys	Leu	Leu	Met	Pro	Gln	Cys		
			100					105					110				
aac	caa	gtg	ctt	gac	gac	tac	ttc	ccc	ctg	gtc	atc	gac	tac	ttc	cag		384
Asn	Gln	Val	Leu	Asp	Asp	Tyr	Phe	Pro	Leu	Val	Ile	Asp	Tyr	Phe	Gln		
		115					120					125					
aac	cag	act	gac	tca	aac	ggc	atc	tgt	atg	cac	ctg	ggc	ctg	tgc	aaa		432
Asn	Gln	Thr	Asp	Ser	Asn	Gly	Ile	Cys	Met	His	Leu	Gly	Leu	Cys	Lys		
	130					135					140						
tcc	cgg	cag	cca	gag	cca	gag	cag	gag	cca	ggg	atg	tca	gac	ccc	ctg		480

Ser 145	Arg	Gln	Pro	Glu	Pro 150	Glu	Gln	Glu	Pro	Gly 155	Met	Ser	Asp	Pro	Leu 160	
ccc Pro	aaa Lys	cct Pro	ctg Leu	cgg Arg 165	gac Asp	cct Pro	ctg Leu	cca Pro	gac Asp 170	cct Pro	ctg Leu	ctg Leu	gac Asp	aag Lys 175	ctc Leu	528
gtc Val	ctc Leu	cct Pro	gtg Val 180	ctg Leu	ccc Pro	ggg Gly	gcc Ala	ctc Leu 185	cag Gln	gcg Ala	agg Arg	cct Pro	ggg Gly 190	cct Pro	cac His	576
aca Thr	cag Gln	gat Asp 195	ctc Leu	tcc Ser	gag Glu	cag Gln	caa Gln 200	ttc Phe	ccc Pro	att Ile	cct Pro	ctc Leu 205	ccc Pro	tat Tyr	tgc Cys	624
tgg Trp	ctc Leu 210	tgc Cys	agg Arg	gct Ala	ctg Leu	atc Ile 215	aag Lys	cgg Arg	atc Ile	caa Gln	gcc Ala 220	atg Met	att Ile	ccc Pro	aag Lys	672
ggt Gly 225	gcg Ala	cta Leu	gct Ala	gtg Val	gca Ala 230	gtg Val	gcc Ala	cag Gln	gtg Val	tgc Cys 235	cgc Arg	gtg Val	gta Val	cct Pro	ctg Leu 240	720
gtg Val	gcg Ala	ggc Gly	ggc Gly	atc Ile 245	tgc Cys	cag Gln	tgc Cys	ctg Leu	gct Ala 250	gag Glu	cgc Arg	tac Tyr	tcc Ser	gtc Val 255	atc Ile	768
ctg Leu	ctc Leu	gac Asp	acg Thr 260	ctg Leu	ctg Leu	ggc Gly	cgc Arg	atg Met 265	ctg Leu	ccc Pro	cag Gln	ctg Leu	gtc Val 270	tgc Cys	cgc Arg	816
ctc Leu	gtc Val	ctc Leu 275	cgg Arg	tgc Cys	tcc Ser	atg Met	cag Gln 280	ata Ile	tct Ser	aag Lys	ccc Pro	tcc Ser 285	tct Ser	cct Pro	cca Pro	864
gaa Glu	gaa Glu 290	tta Leu	aaa Lys	ttt Phe	cag Gln	tgt Cys 295	ggc Gly	caa Gln	aag Lys	act Thr	ctg Leu 300	agg Arg	ccc Pro	cgc Arg	ttt Phe	912
aag Lys 305	att Ile	att Ile	ggg Gly	gga Gly	gaa Glu 310	ttc Phe	acc Thr	acc Thr	atc Ile	gag Glu 315	aac Asn	cag Gln	ccc Pro	tgg Trp	ttt Phe 320	960
gcg Ala	gcc Ala	atc Ile	tac Tyr	agg Arg 325	agg Arg	cac His	cgg Arg	ggg Gly	ggc Gly 330	tct Ser	gtc Val	acc Thr	tac Tyr	gtg Val 335	tgt Cys	1008
gga Gly	ggc Gly	agc Ser	ctc Leu 340	atc Ile	agc Ser	cct Pro	tgc Cys	tgg Trp 345	gtg Val	atc Ile	agc Ser	gcc Ala	aca Thr 350	cac His	tgc Cys	1056
ttc Phe	att Ile	gat Asp 355	tac Tyr	cca Pro	aag Lys	aag Lys	gag Glu 360	gac Asp	tac Tyr	atc Ile	gtc Val	tac Tyr 365	ctg Leu	ggt Gly	cgc Arg	1104
tca Ser	agg Arg 370	ctt Leu	aac Asn	tcc Ser	aac Asn	acg Thr 375	caa Gln	ggg Gly	gag Glu	atg Met	aag Lys 380	ttt Phe	gag Glu	gtg Val	gaa Glu	1152
aac	ctc	atc	cta	cac	aag	gac	tac	agc	gct	gac	acg	ctt	gct	cac	cac	1200

Asn 385	Leu	Ile	Leu	His	Lys 390	Asp	Tyr	Ser	Ala	Asp 395	Thr	Leu	Ala	His	His 400	
aac Asn	gac Asp	att Ile	gcc Ala	ttg Leu 405	ctg Leu	aag Lys	atc Ile	cgt Arg	tcc Ser 410	aag Lys	gag Glu	ggc Gly	agg Arg	tgt Cys 415	gcg Ala	1248
cag Gln	cca Pro	tcc Ser	cgg Arg 420	act Thr	ata Ile	cag Gln	acc Thr	atc Ile 425	tgc Cys	ctg Leu	ccc Pro	tcg Ser	atg Met 430	tat Tyr	aac Asn	1296
gat Asp	ccc Pro	cag Gln 435	ttt Phe	ggc Gly	aca Thr	agc Ser	tgt Cys 440	gag Glu	atc Ile	act Thr	ggc Gly	ttt Phe 445	gga Gly	aaa Lys	gag Glu	1344
aat Asn	tct Ser 450	acc Thr	gac Asp	tat Tyr	ctc Leu	tat Tyr 455	ccg Pro	gag Glu	cag Gln	ctg Leu	aaa Lys 460	atg Met	act Thr	gtt Val	gtg Val	1392
aag Lys 465	ctg Leu	att Ile	tcc Ser	cac His	cgg Arg 470	gag Glu	tgt Cys	cag Gln	cag Gln	ccc Pro 475	cac His	tac Tyr	tac Tyr	ggc Gly	tct Ser 480	1440
gaa Glu	gtc Val	acc Thr	acc Thr	aaa Lys 485	atg Met	ctg Leu	tgt Cys	gct Ala	gct Ala 490	gac Asp	cca Pro	cag Gln	tgg Trp	aaa Lys 495	aca Thr	1488
gat Asp	tcc Ser	tgc Cys	cag Gln 500	gga Gly	gac Asp	tca Ser	ggg Gly	gga Gly 505	ccc Pro	ctc Leu	gtc Val	tgt Cys	tcc Ser 510	ctc Leu	caa Gln	1536
ggc Gly	cgc Arg	atg Met 515	act Thr	ttg Leu	act Thr	gga Gly	att Ile 520	gtg Val	agc Ser	tgg Trp	ggc Gly	cgt Arg 525	gga Gly	tgt Cys	gcc Ala	1584
ctg Leu	aag Lys 530	gac Asp	aag Lys	cca Pro	ggc Gly	gtc Val 535	tac Tyr	acg Thr	aga Arg	gtc Val	tca Ser 540	cac His	ttc Phe	tta Leu	ccc Pro	1632
tgg Trp 545	atc Ile	cgc Arg	agt Ser	cac His	acc Thr 550	aag Lys	gaa Glu	gag Gln	aat Asn	ggc Gly 555	ctg Leu	gcc Ala	ctc Leu			1674
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<211>	591															
<212>	DNA															
<213>	Homo sapiens															
<220>																
<221>	CDS															
<222>	(1) ... (591)															
<223>	Coding sequence of the surfactant protein C precursor															
<400>	8															
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tcc gca gct ccc cgg ggc cga ttt ggc att ccc tgc tgc cca gtg cac	96
Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His	
20 25 30	
ctg aaa cgc ctt ctt atc gtg gtg gtg gtg gtg gtc ctc atc gtc gtg	144
Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Ile Val Val	
35 40 45	
gtg att gtg gga gcc ctg ctc atg ggt ctc cac atg agc cag aaa cac	192
Val Ile Val Gly Ala Leu Leu Met Gly Leu His Met Ser Gln Lys His	
50 55 60	
acg gag atg gtt ctg gag atg agc att ggg gcg ccg gaa gcc cag caa	240
Thr Glu Met Val Leu Glu Met Ser Ile Gly Ala Pro Glu Ala Gln Gln	
65 70 75 80	
cgc ctg gcc ctg agt gag cac ctg gtt acc act gcc acc ttc tcc atc	288
Arg Leu Ala Leu Ser Glu His Leu Val Thr Thr Ala Thr Phe Ser Ile	
85 90 95	
ggc tcc act ggc ctc gtg gtg tat gac tac cag cag ctg ctg atc gcc	336
Gly Ser Thr Gly Leu Val Val Tyr Asp Tyr Gln Gln Leu Leu Ile Ala	
100 105 110	
tac aag cca gcc cct ggc acc tgc tgc tac atc atg aag ata gct cca	384
Tyr Lys Pro Ala Pro Gly Thr Cys Cys Tyr Ile Met Lys Ile Ala Pro	
115 120 125	
gag agc atc ccc agt ctt gag gct ctc act aga aaa gtc cac aac ttc	432
Glu Ser Ile Pro Ser Leu Glu Ala Leu Thr Arg Lys Val His Asn Phe	
130 135 140	
cag atg gaa tgc tct ctg cag gcc aag ccc gca gtg cct acg tct aag	480
Gln Met Glu Cys Ser Leu Gln Ala Lys Pro Ala Val Pro Thr Ser Lys	
145 150 155 160	
ctg ggc cag gca gag ggg cga gat gca ggc tca gca ccc tcc gga ggg	528
Leu Gly Gln Ala Glu Gly Arg Asp Ala Gly Ser Ala Pro Ser Gly Gly	
165 170 175	
gac ccg gcc ttc ctg ggc atg gcc gtg agc acc ctg tgt ggc gag gtg	576
Asp Pro Ala Phe Leu Gly Met Ala Val Ser Thr Leu Cys Gly Glu Val	
180 185 190	
ccg ctc tac tac atc	591
Pro Leu Tyr Tyr Ile	
195	
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<211> 174	
<212> DNA	
<213> Homo sapiens	
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<221> CDS	
<222> (1) ... (174)	
<223> Coding sequence of SP-C precursor lacking the C-terminal propeptide	
<400> 9	

atg gat gtg ggc agc aaa gag gtc ctg atg gag agc ccg ccg gac tac	48
Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr	
1 5 10 15	
tcc gca gct ccc cgg ggc cga ttt ggc att ccc tgc tgc cca gtg cac	96
Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His	
20 25 30	
ctg aaa cgc ctt ctt atc gtg gtg gtg gtg gtg gtc ctc atc gtc gtg	144
Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Ile Val Val	
35 40 45	
gtg att gtg gga gcc ctg ctc atg ggt ctc	174
Val Ile Val Gly Ala Leu Leu Met Gly Leu	
50 55	

<210> 10  
 <211> 105  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) ... (105)  
 <223> Coding sequence of the mature surfactant protein C

<400> 10

ttt ggc att ccc tgc tgc cca gtg cac ctg aaa cgc ctt ctt atc gtg	48
Phe Gly Ile Pro Cys Cys Pro Val His Leu Lys Arg Leu Leu Ile Val	
1 5 10 15	
gtg gtg gtg gtg gtc ctc atc gtc gtg gtg att gtg gga gcc ctg ctc	96
Val Val Val Val Val Leu Ile Val Val Val Ile Val Gly Ala Leu Leu	
20 25 30	
atg ggt ctc	105
Met Gly Leu	
35	

<210> 11  
 <211> 1686  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) ... (1686)  
 <223> Coding sequence of the tissue-plasminogen activator

<400> 11

atg gat gca atg aag aga ggg ctc tgc tgt gtg ctg ctg ctg tgt gga	48
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly	
1 5 10 15	
gca gtc ttc gtt tcg ccc agc cag gaa atc cat gcc cga ttc aga aga	96

Ala	Val	Phe	Val 20	Ser	Pro	Ser	Gln	Glu 25	Ile	His	Ala	Arg	Phe 30	Arg	Arg	
gga Gly	gcc Ala	aga Arg 35	tct Ser	tac Tyr	caa Gln	gtg Val	atc Ile 40	tgc Cys	aga Arg	gat Asp	gaa Glu	aaa Lys 45	acg Thr	cag Gln	atg Met	144
ata Ile	tac Tyr 50	cag Gln	caa Gln	cat His	cag Gln	tca Ser 55	tgg Trp	ctg Leu	cgc Arg	cct Pro	gtg Val 60	ctc Leu	aga Arg	agc Ser	aac Asn	192
cgg Arg 65	gtg Val	gaa Glu	tat Tyr	tgc Cys	tgg Trp 70	tgc Cys	aac Asn	agt Ser	ggc Gly	agg Arg 75	gca Ala	cag Gln	tgc Cys	cac His	tca Ser 80	240
gtg Val	cct Pro	gtc Val	aaa Lys	agt Ser 85	tgc Cys	agc Ser	gag Glu	cca Pro	agg Arg 90	tgt Cys	ttc Phe	aac Asn	ggg Gly	ggc Gly 95	acc Thr	288
tgc Cys	cag Gln	cag Gln	gcc Ala 100	ctg Leu	tac Tyr	ttc Phe	tca Ser	gat Asp 105	ttc Phe	gtg Val	tgc Cys	cag Gln	tgc Cys 110	ccc Pro	gaa Glu	336
gga Gly	ttt Phe	gct Ala 115	ggg Gly	aag Lys	tgc Cys	tgt Cys	gaa Glu 120	ata Ile	gat Asp	acc Thr	agg Arg	gcc Ala 125	acg Thr	tgc Cys	tac Tyr	384
gag Glu	gac Asp 130	cag Gln	ggc Gly	atc Ile	agc Ser	tac Tyr 135	agg Arg	ggc Gly	acg Thr	tgg Trp	agc Ser 140	aca Thr	gcg Ala	gag Glu	agt Ser	432
ggc Gly 145	gcc Ala	gag Glu	tgc Cys	acc Thr	aac Asn 150	tgg Trp	aac Asn	agc Ser	agc Ser	gcg Ala 155	ttg Leu	gcc Ala	cag Gln	aag Lys	ccc Pro 160	480
tac Tyr	agc Ser	ggg Gly	cgg Arg	agg Arg 165	cca Pro	gat Asp	gcc Ala	atc Ile	agg Arg 170	ctg Leu	ggc Gly	ctg Leu	ggg Gly	aac Asn 175	cac His	528
aac Asn	tac Tyr	tgc Cys	aga Arg 180	aac Asn	cca Pro	gat Asp	cga Arg	gac Asp 185	tca Ser	aag Lys	ccc Pro	tgg Trp	tgc Cys 190	tac Tyr	gtc Val	576
ttt Phe	aag Lys	gcg Ala 195	ggg Gly	aag Lys	tac Tyr	agc Ser	tca Ser 200	gag Glu	ttc Phe	tgc Cys	agc Ser	acc Thr 205	cct Pro	gcc Ala	tgc Cys	624
tct Ser	gag Glu 210	gga Gly	aac Asn	agt Ser	gac Asp	tgc Cys 215	tac Tyr	ttt Phe	ggg Gly	aat Asn	ggg Gly 220	tca Ser	gcc Ala	tac Tyr	cgt Arg	672
ggc Gly 225	acg Thr	cac His	agc Ser	ctc Leu	acc Thr 230	gag Glu	tcg Ser	ggt Gly	gcc Ala	tcc Ser 235	tgc Cys	ctc Leu	ccg Pro	tgg Trp	aat Asn 240	720
tcc Ser	atg Met	atc Ile	ctg Leu	ata Ile 245	ggc Gly	aag Lys	gtt Val	tac Tyr	aca Thr 250	gca Ala	cag Gln	aac Asn	ccc Pro	agt Ser 255	gcc Ala	768
cag	gca	ctg	ggc	ctg	ggc	aaa	cat	aat	tac	tgc	cgg	aat	cct	gat	ggg	816

Gln	Ala	Leu	Gly 260	Leu	Gly	Lys	His	Asn 265	Tyr	Cys	Arg	Asn	Pro 270	Asp	Gly	
gat Asp	gcc Ala	aag Lys 275	ccc Pro	tgg Trp	tgc Cys	cac His	gtg Val 280	ctg Leu	aag Lys	aac Asn	cgc Arg	agg Arg 285	ctg Leu	acg Thr	tgg Trp	864
gag Glu	tac Tyr 290	tgt Cys	gat Asp	gtg Val	ccc Pro	tcc Ser 295	tgc Cys	tcc Ser	acc Thr	tgc Cys	ggc Gly 300	ctg Leu	aga Arg	cag Gln	tac Tyr	912
agc Ser 305	cag Gln	cct Pro	cag Gln	ttt Phe	cgc Arg 310	atc Ile	aaa Lys	gga Gly	ggg Gly	ctc Leu 315	ttc Phe	gcc Ala	gac Asp	atc Ile	gcc Ala 320	960
tcc Ser	cac His	ccc Pro	tgg Trp	cag Gln 325	gct Ala	gcc Ala	atc Ile	ttt Phe	gcc Ala 330	aag Lys	cac His	agg Arg	agg Arg	tcg Ser 335	ccc Pro	1008
gga Gly	gag Glu	cgg Arg	ttc Phe 340	ctg Leu	tgc Cys	ggg Gly	ggc Gly	ata Ile 345	ctc Leu	atc Ile	agc Ser	tcc Ser	tgc Cys 350	tgg Trp	att Ile	1056
ctc Leu	tct Ser	gcc Ala 355	gcc Ala	cac His	tgc Cys	ttc Phe	cag Gln 360	gag Glu	agg Arg	ttt Phe	ccg Pro	ccc Pro 365	cac His	cac His	ctg Leu	1104
acg Thr	gtg Val 370	atc Ile	ttg Leu	ggc Gly	aga Arg	aca Thr 375	tac Tyr	cgg Arg	gtg Val	gtc Val	cct Pro 380	ggc Gly	gag Glu	gag Glu	gag Glu	1152
cag Gln 385	aaa Lys	ttt Phe	gaa Glu	gtc Val	gaa Glu 390	aaa Lys	tac Tyr	att Ile	gtc Val	cat His 395	aag Lys	gaa Glu	ttc Phe	gat Asp	gat Asp 400	1200
gac Asp	act Thr	tac Tyr	gac Asp	aat Asn 405	gac Asp	att Ile	gcg Ala	ctg Leu	ctg Leu 410	cag Gln	ctg Leu	aaa Lys	tcg Ser	gat Asp 415	tcg Ser	1248
tcc Ser	cgc Arg	tgt Cys	gcc Ala 420	cag Gln	gag Glu	agc Ser	agc Ser	gtg Val 425	gtc Val	cgc Arg	act Thr	gtg Val	tgc Cys 430	ctt Leu	ccc Pro	1296
ccg Pro	gcg Ala	gac Asp 435	ctg Leu	cag Gln	ctg Leu	ccg Pro	gac Asp 440	tgg Trp	acg Thr	gag Glu	tgt Cys	gag Glu 445	ctc Leu	tcc Ser	ggc Gly	1344
tac Tyr	ggc Gly 450	aag Lys	cat His	gag Glu	gcc Ala	ttg Leu 455	tct Ser	cct Pro	ttc Phe	tat Tyr	tcg Ser 460	gag Glu	cgg Arg	ctg Leu	aag Lys	1392
gag Glu 465	gct Ala	cat His	gtc Val	aga Arg	ctg Leu 470	tac Tyr	cca Pro	tcc Ser	agc Ser	cgc Arg 475	tgc Cys	aca Thr	tca Ser	caa Gln	cat His 480	1440
tta Leu	ctt Leu	aac Asn	aga Arg	aca Thr 485	gtc Val	acc Thr	gac Asp	aac Asn	atg Met 490	ctg Leu	tgt Cys	gct Ala	gga Gly	gac Asp 495	act Thr	1488
cgg	agc	ggc	ggg	ccc	cag	gca	aac	ttg	cac	gac	gcc	tgc	cag	ggc	gat	1536

Arg	Ser	Gly	Gly	Pro	Gln	Ala	Asn	Leu	His	Asp	Ala	Cys	Gln	Gly	Asp		
			500					505					510				
tcg	gga	ggc	ccc	ctg	gtg	tgt	ctg	aac	gat	ggc	cgc	atg	act	ttg	gtg		1584
Ser	Gly	Gly	Pro	Leu	Val	Cys	Leu	Asn	Asp	Gly	Arg	Met	Thr	Leu	Val		
		515					520					525					
ggc	atc	atc	agc	tgg	ggc	ctg	ggc	tgt	gga	cag	aag	gat	gtc	ccg	ggt		1632
Gly	Ile	Ile	Ser	Trp	Gly	Leu	Gly	Cys	Gly	Gln	Lys	Asp	Val	Pro	Gly		
	530					535					540						
gtg	tac	acc	aag	gtt	acc	aac	tac	cta	gac	tgg	att	cgt	gac	aac	atg		1680
Val	Tyr	Thr	Lys	Val	Thr	Asn	Tyr	Leu	Asp	Trp	Ile	Arg	Asp	Asn	Met		
	545				550					555					560		
cga	ccg																1686
Arg	Pro																

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 <222> (76) ... (312)  
 <223> Coding sequence of the mature human surfactant protein B

<220>  
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 <222> (313) ... (1140)  
 <223> Coding sequence of human low mw two-chain urokinase-plasminogen activator

<220>  
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 <222> (1141) ... (1158)  
 <223> Hexahistidine affinity tag

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Met	Ala	Glu	Ser	His	Leu	Leu	Gln	Trp	Leu	Leu	Leu	Leu	Leu	Pro	Thr		
	1			5				10						15			
ctc	tgt	ggc	cca	ggc	act	gct	gcc	tgg	ttc	ccc	att	cct	ctc	ccc	tat		96
Leu	Cys	Gly	Pro	Gly	Thr	Ala	Ala	Trp	Phe	Pro	Ile	Pro	Leu	Pro	Tyr		
			20					25					30				
tgc	tgg	ctc	tgc	agg	gct	ctg	atc	aag	cgg	atc	caa	gcc	atg	att	ccc		144
Cys	Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys	Arg	Ile	Gln	Ala	Met	Ile	Pro		
		35					40					45					
aag	ggt	gcg	cta	gct	gtg	gca	gtg	gcc	cag	gtg	tgc	cgc	gtg	gta	cct		192

Lys	Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	Gln	Val	Cys	Arg	Val	Val	Pro	
	50					55					60					
ctg	gtg	gcg	ggc	ggc	atc	tgc	cag	tgc	ctg	gct	gag	cgc	tac	tcc	gtc	240
Leu	Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	Leu	Ala	Glu	Arg	Tyr	Ser	Val	
	65				70					75					80	
atc	ctg	ctc	gac	acg	ctg	ctg	ggc	cgc	atg	ctg	ccc	cag	ctg	gtc	tgc	288
Ile	Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val	Cys	
				85					90					95		
cgc	ctc	gtc	ctc	cgg	tgc	tcc	atg	aag	ccc	tcc	tct	cct	cca	gaa	gaa	336
Arg	Leu	Val	Leu	Arg	Cys	Ser	Met	Lys	Pro	Ser	Ser	Pro	Pro	Glu	Glu	
			100					105					110			
tta	aaa	ttt	cag	tgt	ggc	caa	aag	act	ctg	agg	ccc	cgc	ttt	aag	att	384
Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	Phe	Lys	Ile	
		115					120					125				
att	ggg	gga	gaa	ttc	acc	acc	atc	gag	aac	cag	ccc	tgg	ttt	gcg	gcc	432
Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro	Trp	Phe	Ala	Ala	
	130					135					140					
atc	tac	agg	agg	cac	cgg	ggg	ggc	tct	gtc	acc	tac	gtg	tgt	gga	ggc	480
Ile	Tyr	Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	Cys	Gly	Gly	
	145				150					155					160	
agc	ctc	atc	agc	cct	tgc	tgg	gtg	atc	agc	gcc	aca	cac	tgc	ttc	att	528
Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys	Phe	Ile	
				165					170					175		
gat	tac	cca	aag	aag	gag	gac	tac	atc	gtc	tac	ctg	ggt	cgc	tca	agg	576
Asp	Tyr	Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu	Gly	Arg	Ser	Arg	
			180					185					190			
ctt	aac	tcc	aac	acg	caa	ggg	gag	atg	aag	ttt	gag	gtg	gaa	aac	ctc	624
Leu	Asn	Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	Glu	Asn	Leu	
		195				200					205					
atc	cta	cac	aag	gac	tac	agc	gct	gac	acg	ctt	gct	cac	cac	aac	gac	672
Ile	Leu	His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	His	Asn	Asp	
	210					215					220					
att	gcc	ttg	ctg	aag	atc	cgt	tcc	aag	gag	ggc	agg	tgt	gcg	cag	cca	720
Ile	Ala	Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	Ala	Gln	Pro	
	225				230					235					240	
tcc	cgg	act	ata	cag	acc	atc	tgc	ctg	ccc	tcg	atg	tat	aac	gat	ccc	768
Ser	Arg	Thr	Ile	Gln	Thr	Ile	Cys	Leu	Pro	Ser	Met	Tyr	Asn	Asp	Pro	
				245					250					255		
cag	ttt	ggc	aca	agc	tgt	gag	atc	act	ggc	ttt	gga	aaa	gag	aat	tct	816
Gln	Phe	Gly	Thr	Ser	Cys	Glu	Ile	Thr	Gly	Phe	Gly	Lys	Glu	Asn	Ser	
			260					265					270			
acc	gac	tat	ctc	tat	ccg	gag	cag	ctg	aaa	atg	act	gtt	gtg	aag	ctg	864
Thr	Asp	Tyr	Leu	Tyr	Pro	Glu	Gln	Leu	Lys	Met	Thr	Val	Val	Lys	Leu	
		275					280					285				
att	tcc	cac	cgg	gag	tgt	cag	cag	ccc	cac	tac	tac	ggc	tct	gaa	gtc	912

Ile	Ser	His	Arg	Glu	Cys	Gln	Gln	Pro	His	Tyr	Tyr	Gly	Ser	Glu	Val		
	290					295					300						
acc	acc	aaa	atg	ctg	tgt	gct	gct	gac	cca	cag	tgg	aaa	aca	gat	tcc		960
Thr	Thr	Lys	Met	Leu	Cys	Ala	Ala	Asp	Pro	Gln	Trp	Lys	Thr	Asp	Ser		
305					310					315					320		
tgc	cag	gga	gac	tca	ggg	gga	ccc	ctc	gtc	tgt	tcc	ctc	caa	ggc	cgc		1008
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Ser	Leu	Gln	Gly	Arg		
				325					330					335			
atg	act	ttg	act	gga	att	gtg	agc	tgg	ggc	cgt	gga	tgt	gcc	ctg	aag		1056
Met	Thr	Leu	Thr	Gly	Ile	Val	Ser	Trp	Gly	Arg	Gly	Cys	Ala	Leu	Lys		
			340					345					350				
gac	aag	cca	ggc	gtc	tac	acg	aga	gtc	tca	cac	ttc	tta	ccc	tgg	atc		1104
Asp	Lys	Pro	Gly	Val	Tyr	Thr	Arg	Val	Ser	His	Phe	Leu	Pro	Trp	Ile		
		355					360					365					
cgc	agt	cac	acc	aag	gaa	gag	aat	ggc	ctg	gcc	ctc	cat	cat	cat	cat		1152
Arg	Ser	His	Thr	Lys	Glu	Gln	Asn	Gly	Leu	Ala	Leu	His	His	His	His		
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cat	cat																1158
His	His																
385																	
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<212>	DNA																
<213>	Artificial Sequence																
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<222>	(1) ... (60)																
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<222>	(67) ... (894)																
<223>	Coding sequence of human low mw two-chain urokinase-plasminogen activator																
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<222>	(895) ... (1131)																
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atg	aga	gcc	ctg	ctg	gcg	cgc	ctg	ctt	ctc	tgc	gtc	ctg	gtc	gtg	agc		48
Met	Arg	Ala	Leu	Leu	Ala	Arg	Leu	Leu	Leu	Cys	Val	Leu	Val	Val	Ser		
1				5					10					15			

gac Asp	tcc Ser	aaa Lys	ggc Gly 20	agc Ser	aat Asn	aag Lys	ccc Pro	tcc Ser 25	tct Ser	cct Pro	cca Pro	gaa Glu	gaa Glu 30	tta Leu	aaa Lys	96
ttt Phe	cag Gln	tgt Cys 35	ggc Gly	caa Gln	aag Lys	act Thr	ctg Leu 40	agg Arg	ccc Pro	cgc Arg	ttt Phe	aag Lys 45	att Ile	att Ile	ggg Gly	144
gga Gly	gaa Glu 50	ttc Phe	acc Thr	acc Thr	atc Ile	gag Glu 55	aac Asn	cag Gln	ccc Pro	tgg Trp	ttt Phe 60	gcg Ala	gcc Ala	atc Ile	tac Tyr	192
agg Arg 65	agg Arg	cac His	cgg Arg	ggg Gly	ggc Gly 70	tct Ser	gtc Val	acc Thr	tac Tyr	gtg Val 75	tgt Cys	gga Gly	ggc Gly	agc Ser	ctc Leu 80	240
atc Ile	agc Ser	cct Pro	tgc Cys	tgg Trp 85	gtg Val	atc Ile	agc Ser	gcc Ala	aca Thr 90	cac His	tgc Cys	ttc Phe	att Ile	gat Asp 95	tac Tyr	288
cca Pro	aag Lys	aag Lys	gag Glu 100	gac Asp	tac Tyr	atc Ile	gtc Val	tac Tyr 105	ctg Leu	ggc Gly	cgc Arg	tca Ser	agg Arg 110	ctt Leu	aac Asn	336
tcc Ser	aac Asn	acg Thr 115	caa Gln	ggg Gly	gag Glu	atg Met	aag Lys 120	ttt Phe	gag Glu	gtg Val	gaa Glu	aac Asn 125	ctc Leu	atc Ile	cta Leu	384
cac His	aag Lys 130	gac Asp	tac Tyr	agc Ser	gct Ala	gac Asp 135	acg Thr	ctt Leu	gct Ala	cac His	cac His 140	aac Asn	gac Asp	att Ile	gcc Ala	432
ttg Leu 145	ctg Leu	aag Lys	atc Ile	cgt Arg	tcc Ser 150	aag Lys	gag Glu	ggc Gly	agg Arg	tgt Cys 155	gcg Ala	cag Gln	cca Pro	tcc Ser	cgg Arg 160	480
act Thr	ata Ile	cag Gln	acc Thr	atc Ile 165	tgc Cys	ctg Leu	ccc Pro	tcg Ser	atg Met 170	tat Tyr	aac Asn	gat Asp	ccc Pro	cag Gln 175	ttt Phe	528
ggc Gly	aca Thr	agc Ser	tgt Cys 180	gag Glu	atc Ile	act Thr	ggc Gly	ttt Phe 185	gga Gly	aaa Lys	gag Glu	aac Asn	tct Ser 190	acc Thr	gac Asp	576
tat Tyr	ctc Leu	tat Tyr 195	ccg Pro	gag Glu	cag Gln	ctg Leu	aaa Lys 200	atg Met	act Thr	gtt Val	gtg Val	aag Lys 205	ctg Leu	att Ile	tcc Ser	624
cac His	cgg Arg 210	gag Glu	tgt Cys	cag Gln	cag Gln	ccc Pro 215	cac His	tac Tyr	tac Tyr	ggc Gly	tct Ser 220	gaa Glu	gtc Val	acc Thr	acc Thr	672
aaa Lys 225	atg Met	ctg Leu	tgt Cys	gct Ala	gct Ala 230	gac Asp	cca Pro	cag Gln	tgg Trp	aaa Lys 235	aca Thr	gat Asp	tcc Ser	tgc Cys	cag Gln 240	720
gga Gly	gac Asp	tca Ser	ggg Gly	gga Gly 245	ccc Pro	ctc Leu	gtc Val	tgt Cys	tcc Ser 250	ctc Leu	caa Gln	ggc Gly	cgc Arg	atg Met 255	act Thr	768

ttg act gga att gtg agc tgg ggc cgt gga tgt gcc ctg aag gac aag	816
Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys	
	260
cca ggc gtc tac acg aga gtc tca cac ttc tta ccc tgg atc cgc agt	864
Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg Ser	
	275
cca ggc gtc tac acg aga gtc tca cac ttc tta ccc tgg atc cgc agt	864
Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg Ser	
	280
cac acc aag gaa gag aat ggc ctg gcc ctc ttc ccc att cct ctc ccc	912
His Thr Lys Glu Gln Asn Gly Leu Ala Leu Phe Pro Ile Pro Leu Pro	
	290
cac acc aag gaa gag aat ggc ctg gcc ctc ttc ccc att cct ctc ccc	912
His Thr Lys Glu Gln Asn Gly Leu Ala Leu Phe Pro Ile Pro Leu Pro	
	300
tat tgc tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att	960
Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile	
	305
tat tgc tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att	960
Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile	
	310
ccc aag ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta	1008
Pro Lys Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val	
	325
ccc aag ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta	1008
Pro Lys Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val	
	330
cct ctg gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc	1056
Pro Leu Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser	
	340
cct ctg gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc	1056
Pro Leu Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser	
	345
gtc atc ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc	1104
Val Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val	
	355
gtc atc ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc	1104
Val Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val	
	360
tgc cgc ctc gtc ctc cgg tgc tcc atg cat cat cat cat cat cat	1149
Cys Arg Leu Val Leu Arg Cys Ser Met His His His His His His	
	370
tgc cgc ctc gtc ctc cgg tgc tcc atg cat cat cat cat cat cat	1149
Cys Arg Leu Val Leu Arg Cys Ser Met His His His His His His	
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Cys Arg Leu Val Leu Arg Cys Ser Met His His His His His His	
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 <212> PRT  
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<220>

<221> PEPTIDE  
 <222> (1) ... (381)  
 <223> Surfactant protein B precursor

<400> 14

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			20					25					30		
Ala	Gln	Gly	Pro	Glu	Phe	Trp	Cys	Gln	Ser	Leu	Glu	Gln	Ala	Leu	Gln
		35					40					45			
Cys	Arg	Ala	Leu	Gly	His	Cys	Leu	Gln	Glu	Val	Trp	Gly	His	Val	Gly
	50					55					60				
Ala	Asp	Asp	Leu	Cys	Gln	Glu	Cys	Glu	Asp	Ile	Val	His	Ile	Leu	Asn
65					70					75					80

Lys	Met	Ala	Lys	Glu <sub>85</sub>	Ala	Ile	Phe	Gln	Asp <sub>90</sub>	Thr	Met	Arg	Lys	Phe <sub>95</sub>	Leu
Glu	Gln	Glu	Cys <sub>100</sub>	Asn	Val	Leu	Pro	Leu <sub>105</sub>	Lys	Leu	Leu	Met	Pro <sub>110</sub>	Gln	Cys
Asn	Gln	Val <sub>115</sub>	Leu	Asp	Asp	Tyr	Phe <sub>120</sub>	Pro	Leu	Val	Ile	Asp <sub>125</sub>	Tyr	Phe	Gln
Asn	Gln <sub>130</sub>	Thr	Asp	Ser	Asn	Gly <sub>135</sub>	Ile	Cys	Met	His	Leu <sub>140</sub>	Gly	Leu	Cys	Lys
Ser <sub>145</sub>	Arg	Gln	Pro	Glu	Pro <sub>150</sub>	Glu	Gln	Glu	Pro	Gly <sub>155</sub>	Met	Ser	Asp	Pro	Leu <sub>160</sub>
Pro	Lys	Pro	Leu	Arg <sub>165</sub>	Asp	Pro	Leu	Pro	Asp <sub>170</sub>	Pro	Leu	Leu	Asp	Lys <sub>175</sub>	Leu
Val	Leu	Pro	Val <sub>180</sub>	Leu	Pro	Gly	Ala	Leu <sub>185</sub>	Gln	Ala	Arg	Pro	Gly <sub>190</sub>	Pro	His
Thr	Gln	Asp <sub>195</sub>	Leu	Ser	Glu	Gln	Gln <sub>200</sub>	Phe	Pro	Ile	Pro	Leu <sub>205</sub>	Pro	Tyr	Cys
Trp	Leu <sub>210</sub>	Cys	Arg	Ala	Leu	Ile <sub>215</sub>	Lys	Arg	Ile	Gln	Ala <sub>220</sub>	Met	Ile	Pro	Lys
Gly <sub>225</sub>	Ala	Leu	Ala	Val	Ala <sub>230</sub>	Val	Ala	Gln	Val	Cys <sub>235</sub>	Arg	Val	Val	Pro	Leu <sub>240</sub>
Val	Ala	Gly	Gly	Ile <sub>245</sub>	Cys	Gln	Cys	Leu	Ala <sub>250</sub>	Glu	Arg	Tyr	Ser	Val <sub>255</sub>	Ile
Leu	Leu	Asp	Thr <sub>260</sub>	Leu	Leu	Gly	Arg	Met <sub>265</sub>	Leu	Pro	Gln	Leu	Val <sub>270</sub>	Cys	Arg
Leu	Val	Leu <sub>275</sub>	Arg	Cys	Ser	Met	Asp <sub>280</sub>	Asp	Ser	Ala	Gly	Pro <sub>285</sub>	Arg	Ser	Pro
Thr	Gly <sub>290</sub>	Glu	Trp	Leu	Pro	Arg <sub>295</sub>	Asp	Ser	Glu	Cys	His <sub>300</sub>	Leu	Cys	Met	Ser
Val <sub>305</sub>	Thr	Thr	Gln	Ala	Gly <sub>310</sub>	Asn	Ser	Ser	Glu	Gln <sub>315</sub>	Ala	Ile	Pro	Gln	Ala <sub>320</sub>
Met	Leu	Gln	Ala	Cys <sub>325</sub>	Val	Gly	Ser	Trp	Leu <sub>330</sub>	Asp	Arg	Glu	Lys	Cys <sub>335</sub>	Lys
Gln	Phe	Val	Glu <sub>340</sub>	Gln	His	Thr	Pro	Gln <sub>345</sub>	Leu	Leu	Thr	Leu	Val <sub>350</sub>	Pro	Arg
Gly	Trp	Asp <sub>355</sub>	Ala	His	Thr	Thr	Cys <sub>360</sub>	Gln	Ala	Leu	Gly	Val <sub>365</sub>	Cys	Gly	Thr
Met	Ser <sub>370</sub>	Ser	Pro	Leu	Gln	Cys <sub>375</sub>	Ile	His	Ser	Pro	Asp <sub>380</sub>	Leu			

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 <223> Surfactant protein B precursor lacking the C-terminal propeptide  
  
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 Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys  
                   20                  25                  30  
 Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln  
                   35                  40                  45  
 Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly  
   50                  55                  60  
 Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn  
   65                  70                  75                  80  
 Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu  
                   85                  90                  95  
 Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys  
                   100                  105                  110  
 Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln  
                   115                  120                  125  
 Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys  
   130                  135                  140  
 Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu  
   145                  150                  155                  160  
 Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu  
                   165                  170                  175  
 Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His  
                   180                  185                  190  
 Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys  
                   195                  200                  205  
 Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys  
   210                  215                  220  
 Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu  
   225                  230                  235                  240  
 Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile  
                   245                  250                  255  
 Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg

	260	265	270
--	-----	-----	-----

Leu Val Leu Arg Cys Ser Met  
 275

<210> 16  
 <211> 79  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> PEPTIDE  
 <222> (1) ... (79)  
 <223> Mature surfactant protein B  
 <400> 16

Phe Pro Ile Pro Leu Pro Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys  
 1 5 10 15  
 Arg Ile Gln Ala Met Ile Pro Lys Gly Ala Leu Ala Val Ala Val Ala  
 20 25 30  
 Gln Val Cys Arg Val Val Pro Leu Val Ala Gly Gly Ile Cys Gln Cys  
 35 40 45  
 Leu Ala Glu Arg Tyr Ser Val Ile Leu Leu Asp Thr Leu Leu Gly Arg  
 50 55 60  
 Met Leu Pro Gln Leu Val Cys Arg Leu Val Leu Arg Cys Ser Met  
 65 70 75

<210> 17  
 <211> 431  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> PEPTIDE  
 <222> (1) ... (431)  
 <223> Single-chain urokinase-plasminogen activator  
 <400> 17

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser  
 1 5 10 15  
 Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp  
 20 25 30  
 Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile  
 35 40 45  
 His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile  
 50 55 60  
 Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly

65						70						75						80
Lys	Ala	Ser	Thr	Asp <sub>85</sub>	Thr	Met	Gly	Arg	Pro <sub>90</sub>	Cys	Leu	Pro	Trp	Asn <sub>95</sub>	Ser			
Ala	Thr	Val	Leu <sub>100</sub>	Gln	Gln	Thr	Tyr	His <sub>105</sub>	Ala	His	Arg	Ser	Asp <sub>110</sub>	Ala	Leu			
Gln	Leu	Gly <sub>115</sub>	Leu	Gly	Lys	His	Asn <sub>120</sub>	Tyr	Cys	Arg	Asn	Pro <sub>125</sub>	Asp	Asn	Arg			
Arg	Arg <sub>130</sub>	Pro	Trp	Cys	Tyr	Val <sub>135</sub>	Gln	Val	Gly	Leu	Lys <sub>140</sub>	Pro	Leu	Val	Gln			
Glu <sub>145</sub>	Cys	Met	Val	His	Asp <sub>150</sub>	Cys	Ala	Asp	Gly	Lys <sub>155</sub>	Lys	Pro	Ser	Ser	Pro <sub>160</sub>			
Pro	Glu	Glu	Leu	Lys <sub>165</sub>	Phe	Gln	Cys	Gly	Gln <sub>170</sub>	Lys	Thr	Leu	Arg	Pro <sub>175</sub>	Arg			
Phe	Lys	Ile	Ile <sub>180</sub>	Gly	Gly	Glu	Phe	Thr <sub>185</sub>	Thr	Ile	Glu	Asn	Gln <sub>190</sub>	Pro	Trp			
Phe	Ala	Ala <sub>195</sub>	Ile	Tyr	Arg	Arg	His <sub>200</sub>	Arg	Gly	Gly	Ser	Val <sub>205</sub>	Thr	Tyr	Val			
Cys	Gly <sub>210</sub>	Gly	Ser	Leu	Ile	Ser <sub>215</sub>	Pro	Cys	Trp	Val	Ile <sub>220</sub>	Ser	Ala	Thr	His			
Cys <sub>225</sub>	Phe	Ile	Asp	Tyr	Pro <sub>230</sub>	Lys	Lys	Glu	Asp	Tyr <sub>235</sub>	Ile	Val	Tyr	Leu	Gly <sub>240</sub>			
Arg	Ser	Arg	Leu	Asn <sub>245</sub>	Ser	Asn	Thr	Gln	Gly <sub>250</sub>	Glu	Met	Lys	Phe	Glu <sub>255</sub>	Val			
Glu	Asn	Leu	Ile <sub>260</sub>	Leu	His	Lys	Asp	Tyr <sub>265</sub>	Ser	Ala	Asp	Thr	Leu <sub>270</sub>	Ala	His			
His	Asn	Asp <sub>275</sub>	Ile	Ala	Leu	Leu	Lys <sub>280</sub>	Ile	Arg	Ser	Lys	Glu <sub>285</sub>	Gly	Arg	Cys			
Ala	Gln <sub>290</sub>	Pro	Ser	Arg	Thr	Ile <sub>295</sub>	Gln	Thr	Ile	Cys	Leu <sub>300</sub>	Pro	Ser	Met	Tyr			
Asn <sub>305</sub>	Asp	Pro	Gln	Phe	Gly <sub>310</sub>	Thr	Ser	Cys	Glu	Ile <sub>315</sub>	Thr	Gly	Phe	Gly	Lys <sub>320</sub>			
Glu	Asn	Ser	Thr	Asp <sub>325</sub>	Tyr	Leu	Tyr	Pro	Glu <sub>330</sub>	Gln	Leu	Lys	Met	Thr <sub>335</sub>	Val			
Val	Lys	Leu	Ile <sub>340</sub>	Ser	His	Arg	Glu	Cys <sub>345</sub>	Gln	Gln	Pro	His	Tyr <sub>350</sub>	Tyr	Gly			
Ser	Glu	Val <sub>355</sub>	Thr	Thr	Lys	Met	Leu <sub>360</sub>	Cys	Ala	Ala	Asp	Pro <sub>365</sub>	Gln	Trp	Lys			
Thr	Asp <sub>370</sub>	Ser	Cys	Gln	Gly	Asp <sub>375</sub>	Ser	Gly	Gly	Pro	Leu <sub>380</sub>	Val	Cys	Ser	Leu			
Gln	Gly	Arg	Met	Thr	Leu	Thr	Gly	Ile	Val	Ser	Trp	Gly	Arg	Gly	Cys			

385		390		395		400									
Ala	Leu	Lys	Asp	Lys	Pro	Gly	Val	Tyr	Thr	Arg	Val	Ser	His	Phe	Leu
				405					410					415	
Pro	Trp	Ile	Arg	Ser	His	Thr	Lys	Glu	Gln	Asn	Gly	Leu	Ala	Leu	
			420					425					430		

<210> 18  
 <211> 276  
 <212> PRT  
 <213> Homo sapiens  
  
 <220>  
 <221> PEPTIDE  
 <222> (1) ... (276)  
 <223> Low molecular weight two-chain urokinase-plasminogen activator  
  
 <400> 18

Lys	Pro	Ser	Ser	Pro	Pro	Glu	Glu	Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys
1				5					10					15	
Thr	Leu	Arg	Pro	Arg	Phe	Lys	Ile	Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile
			20					25					30		
Glu	Asn	Gln	Pro	Trp	Phe	Ala	Ala	Ile	Tyr	Arg	Arg	His	Arg	Gly	Gly
		35					40					45			
Ser	Val	Thr	Tyr	Val	Cys	Gly	Gly	Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val
	50					55					60				
Ile	Ser	Ala	Thr	His	Cys	Phe	Ile	Asp	Tyr	Pro	Lys	Lys	Glu	Asp	Tyr
65					70					75					80
Ile	Val	Tyr	Leu	Gly	Arg	Ser	Arg	Leu	Asn	Ser	Asn	Thr	Gln	Gly	Glu
				85					90					95	
Met	Lys	Phe	Glu	Val	Glu	Asn	Leu	Ile	Leu	His	Lys	Asp	Tyr	Ser	Ala
			100					105					110		
Asp	Thr	Leu	Ala	His	His	Asn	Asp	Ile	Ala	Leu	Leu	Lys	Ile	Arg	Ser
		115					120					125			
Lys	Glu	Gly	Arg	Cys	Ala	Gln	Pro	Ser	Arg	Thr	Ile	Gln	Thr	Ile	Cys
	130					135					140				
Leu	Pro	Ser	Met	Tyr	Asn	Asp	Pro	Gln	Phe	Gly	Thr	Ser	Cys	Glu	Ile
145					150					155					160
Thr	Gly	Phe	Gly	Lys	Glu	Asn	Ser	Thr	Asp	Tyr	Leu	Tyr	Pro	Glu	Gln
				165					170					175	
Leu	Lys	Met	Thr	Val	Val	Lys	Leu	Ile	Ser	His	Arg	Glu	Cys	Gln	Gln
			180					185					190		
Pro	His	Tyr	Tyr	Gly	Ser	Glu	Val	Thr	Thr	Lys	Met	Leu	Cys	Ala	Ala
		195					200					205			

Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro  
 210 215 220  
 Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser  
 225 230 235 240  
 Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg  
 245 250 255  
 Val Ser His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Gln Asn  
 260 265 270  
 Gly Leu Ala Leu  
 275

<210> 19  
 <211> 557  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> PEPTIDE  
 <222> (1) ... (279)  
 <223> Human surfactant protein B precursor lacking the C-terminal propeptide

<220>  
 <221> PEPTIDE  
 <222> (282) ... (577)  
 <223> Human low molecular weight two-chain urokinase-plasminogen activator

<400> 19

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr  
 1 5 10 15  
 Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys  
 20 25 30  
 Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln  
 35 40 45  
 Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly  
 50 55 60  
 Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn  
 65 70 75 80  
 Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu  
 85 90 95  
 Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys  
 100 105 110  
 Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln  
 115 120 125  
 Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys  
 130 135 140

Ser 145	Arg	Gln	Pro	Glu 150	Pro	Glu	Gln	Glu	Pro	Gly 155	Met	Ser	Asp	Pro	Leu 160
Pro	Lys	Pro	Leu	Arg 165	Asp	Pro	Leu	Pro	Asp 170	Pro	Leu	Leu	Asp	Lys 175	Leu
Val	Leu	Pro	Val 180	Leu	Pro	Gly	Ala	Leu 185	Gln	Ala	Arg	Pro	Gly 190	Pro	His
Thr	Gln	Asp 195	Leu	Ser	Glu	Gln	Gln 200	Phe	Pro	Ile	Pro	Leu 205	Pro	Tyr	Cys
Trp	Leu 210	Cys	Arg	Ala	Leu	Ile 215	Lys	Arg	Ile	Gln	Ala 220	Met	Ile	Pro	Lys
Gly 225	Ala	Leu	Ala	Val	Ala 230	Val	Ala	Gln	Val	Cys 235	Arg	Val	Val	Pro	Leu 240
Val	Ala	Gly	Gly	Ile 245	Cys	Gln	Cys	Leu	Ala 250	Glu	Arg	Tyr	Ser	Val 255	Ile
Leu	Leu	Asp	Thr 260	Leu	Leu	Gly	Arg	Met 265	Leu	Pro	Gln	Leu	Val 270	Cys	Arg
Leu	Val	Leu 275	Arg	Cys	Ser	Met	Lys 280	Leu	Lys	Pro	Ser	Ser 285	Pro	Pro	Glu
Glu 290	Leu	Lys	Phe	Gln	Cys	Gly 295	Gln	Lys	Thr	Leu	Arg 300	Pro	Arg	Phe	Lys
Ile 305	Ile	Gly	Gly	Glu	Phe 310	Thr	Thr	Ile	Glu	Asn 315	Gln	Pro	Trp	Phe	Ala 320
Ala	Ile	Tyr	Arg	Arg 325	His	Arg	Gly	Gly	Ser 330	Val	Thr	Tyr	Val	Cys 335	Gly
Gly	Ser	Leu	Ile 340	Ser	Pro	Cys	Trp	Val 345	Ile	Ser	Ala	Thr	His 350	Cys	Phe
Ile	Asp	Tyr 355	Pro	Lys	Lys	Glu	Asp 360	Tyr	Ile	Val	Tyr	Leu 365	Gly	Arg	Ser
Arg	Leu 370	Asn	Ser	Asn	Thr	Gln 375	Gly	Glu	Met	Lys	Phe 380	Glu	Val	Glu	Asn
Leu 385	Ile	Leu	His	Lys	Asp 390	Tyr	Ser	Ala	Asp	Thr 395	Leu	Ala	His	His	Asn 400
Asp	Ile	Ala	Leu	Leu 405	Lys	Ile	Arg	Ser	Lys 410	Glu	Gly	Arg	Cys	Ala 415	Gln
Pro	Ser	Arg	Thr 420	Ile	Gln	Thr	Ile	Cys 425	Leu	Pro	Ser	Met	Tyr 430	Asn	Asp
Pro	Gln	Phe 435	Gly	Thr	Ser	Cys	Glu 440	Ile	Thr	Gly	Phe	Gly 445	Lys	Glu	Asn
Ser	Thr 450	Asp	Tyr	Leu	Tyr	Pro 455	Glu	Gln	Leu	Lys	Met 460	Thr	Val	Val	Lys

Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu  
 465 470 475 480  
 Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp  
 485 490 495  
 Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly  
 500 505 510  
 Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu  
 515 520 525  
 Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp  
 530 535 540  
 Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu  
 545 550 555

<210> 20  
 <211> 558  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <221> PEPTIDE  
 <222> (1) ... (279)  
 <223> Human surfactant protein B precursor lacking the C-terminal propeptide

<220>  
 <221> PEPTIDE  
 <222> (283) ... (558)  
 <223> Human low molecular weight two-chain urokinase-plasminogen activator

<400> 20

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr  
 1 5 10 15  
 Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys  
 20 25 30  
 Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln  
 35 40 45  
 Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly  
 50 55 60  
 Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn  
 65 70 75 80  
 Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu  
 85 90 95  
 Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys  
 100 105 110  
 Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln

115					120					125					
Asn	Gln	Thr	Asp	Ser	Asn	Gly	Ile	Cys	Met	His	Leu	Gly	Leu	Cys	Lys
130					135					140					
Ser	Arg	Gln	Pro	Glu	Pro	Glu	Gln	Glu	Pro	Gly	Met	Ser	Asp	Pro	Leu
145					150					155					160
Pro	Lys	Pro	Leu	Arg	Asp	Pro	Leu	Pro	Asp	Pro	Leu	Leu	Asp	Lys	Leu
				165					170					175	
Val	Leu	Pro	Val	Leu	Pro	Gly	Ala	Leu	Gln	Ala	Arg	Pro	Gly	Pro	His
			180					185					190		
Thr	Gln	Asp	Leu	Ser	Glu	Gln	Gln	Phe	Pro	Ile	Pro	Leu	Pro	Tyr	Cys
		195					200					205			
Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys	Arg	Ile	Gln	Ala	Met	Ile	Pro	Lys
	210					215					220				
Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	Gln	Val	Cys	Arg	Val	Val	Pro	Leu
225					230					235					240
Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	Leu	Ala	Glu	Arg	Tyr	Ser	Val	Ile
				245					250					255	
Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val	Cys	Arg
			260					265					270		
Leu	Val	Leu	Arg	Cys	Ser	Met	Gln	Ile	Ser	Lys	Pro	Ser	Ser	Pro	Pro
		275					280					285			
Glu	Glu	Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	Phe
	290					295					300				
Lys	Ile	Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro	Trp	Phe
305					310					315					320
Ala	Ala	Ile	Tyr	Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	Cys
				325					330					335	
Gly	Gly	Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys
			340					345					350		
Phe	Ile	Asp	Tyr	Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu	Gly	Arg
		355					360					365			
Ser	Arg	Leu	Asn	Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	Glu
	370					375					380				
Asn	Leu	Ile	Leu	His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	His
385					390					395					400
Asn	Asp	Ile	Ala	Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	Ala
				405					410					415	
Gln	Pro	Ser	Arg	Thr	Ile	Gln	Thr	Ile	Cys	Leu	Pro	Ser	Met	Tyr	Asn
			420					425					430		
Asp	Pro	Gln	Phe	Gly	Thr	Ser	Cys	Glu	Ile	Thr	Gly	Phe	Gly	Lys	Glu

435	440	445		
Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val	450	455	460	
Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser	465	470	475	480
Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr	485	490	495	
Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln	500	505	510	
Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala	515	520	525	
Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro	530	535	540	
Trp Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu	545	550	555	

<210> 21  
 <211> 197  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> PEPTIDE  
 <222> (1) ... (197)  
 <223> Surfactant protein C precursor

<400> 21

Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr	1	5	10	15
Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His	20	25	30	
Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Ile Val Val	35	40	45	
Val Ile Val Gly Ala Leu Leu Met Gly Leu His Met Ser Gln Lys His	50	55	60	
Thr Glu Met Val Leu Glu Met Ser Ile Gly Ala Pro Glu Ala Gln Gln	65	70	75	80
Arg Leu Ala Leu Ser Glu His Leu Val Thr Thr Ala Thr Phe Ser Ile	85	90	95	
Gly Ser Thr Gly Leu Val Val Tyr Asp Tyr Gln Gln Leu Leu Ile Ala	100	105	110	
Tyr Lys Pro Ala Pro Gly Thr Cys Cys Tyr Ile Met Lys Ile Ala Pro	115	120	125	

Glu Ser Ile Pro Ser Leu Glu Ala Leu Thr Arg Lys Val His Asn Phe  
 130 135 140  
 Gln Met Glu Cys Ser Leu Gln Ala Lys Pro Ala Val Pro Thr Ser Lys  
 145 150 155 160  
 Leu Gly Gln Ala Glu Gly Arg Asp Ala Gly Ser Ala Pro Ser Gly Gly  
 165 170 175  
 Asp Pro Ala Phe Leu Gly Met Ala Val Ser Thr Leu Cys Gly Glu Val  
 180 185 190  
 Pro Leu Tyr Tyr Ile  
 195

<210> 22  
 <211> 58  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> PEPTIDE  
 <222> (1) ... (58)  
 <223> Surfactant protein C precursor lacking the C-terminal  
 propeptide

<400> 22

Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr  
 1 5 10 15  
 Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His  
 20 25 30  
 Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Ile Val Val  
 35 40 45  
 Val Ile Val Gly Ala Leu Leu Met Gly Leu  
 50 55

<210> 23  
 <211> 35  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> PEPTIDE  
 <222> (1) ... (35)  
 <223> Mature surfactant protein C

<400> 23

Phe Gly Ile Pro Cys Cys Pro Val His Leu Lys Arg Leu Leu Ile Val  
 1 5 10 15  
 Val Val Val Val Val Leu Ile Val Val Val Ile Val Gly Ala Leu Leu  
 20 25 30

Met Gly Leu  
35

<210> 24  
<211> 562  
<212> PRT  
<213> Homo sapiens

<220>  
<221> PEPTIDE  
<222> (1) ... (562)  
<223> Tissue-plasminogen activator

<400> 24

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly  
1 5 10 15  
Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg  
20 25 30  
Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met  
35 40 45  
Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn  
50 55 60  
Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser  
65 70 75 80  
Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr  
85 90 95  
Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu  
100 105 110  
Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr  
115 120 125  
Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser  
130 135 140  
Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro  
145 150 155 160  
Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His  
165 170 175  
Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val  
180 185 190  
Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys  
195 200 205  
Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg  
210 215 220  
Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn  
225 230 235 240

Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala  
245 250 255  
Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly  
260 265 270  
Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp  
275 280 285  
Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr  
290 295 300  
Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala  
305 310 315 320  
Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro  
325 330 335  
Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile  
340 345 350  
Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu  
355 360 365  
Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu  
370 375 380  
Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp  
385 390 395 400  
Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser  
405 410 415  
Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro  
420 425 430  
Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly  
435 440 445  
Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys  
450 455 460  
Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His  
465 470 475 480  
Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr  
485 490 495  
Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp  
500 505 510  
Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val  
515 520 525  
Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly  
530 535 540  
Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met  
545 550 555 560

Arg Pro

<210> 25  
<211> 386  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> SIGNAL  
<222> (1) ... (23)  
<223> Signal sequence of the human surfactant protein B

<220>  
<221> PEPTIDE  
<222> (26) ... (104)  
<223> Mature human surfactant protein B

<220>  
<221> PEPTIDE  
<222> (105) ... (380)  
<223> Human low molecular weight two-chain urokinase-plasminogen activator

<220>  
<221> PEPTIDE  
<222> (381) ... (386)  
<223> Hexahistidine affinity tag

<400> 25

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr  
1 5 10 15  
Leu Cys Gly Pro Gly Thr Ala Ala Trp Phe Pro Ile Pro Leu Pro Tyr  
20 25 30  
Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro  
35 40 45  
Lys Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro  
50 55 60  
Leu Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val  
65 70 75 80  
Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys  
85 90 95  
Arg Leu Val Leu Arg Cys Ser Met Lys Pro Ser Ser Pro Pro Glu Glu  
100 105 110  
Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile  
115 120 125  
Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala  
130 135 140  
Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly

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Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys	Phe	Ile
				165					170					175	
Asp	Tyr	Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu	Gly	Arg	Ser	Arg
			180					185					190		
Leu	Asn	Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	Glu	Asn	Leu
		195					200					205			
Ile	Leu	His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	His	Asn	Asp
	210					215					220				
Ile	Ala	Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	Ala	Gln	Pro
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Ser	Arg	Thr	Ile	Gln	Thr	Ile	Cys	Leu	Pro	Ser	Met	Tyr	Asn	Asp	Pro
				245					250					255	
Gln	Phe	Gly	Thr	Ser	Cys	Glu	Ile	Thr	Gly	Phe	Gly	Lys	Glu	Asn	Ser
			260					265					270		
Thr	Asp	Tyr	Leu	Tyr	Pro	Glu	Gln	Leu	Lys	Met	Thr	Val	Val	Lys	Leu
		275					280					285			
Ile	Ser	His	Arg	Glu	Cys	Gln	Gln	Pro	His	Tyr	Tyr	Gly	Ser	Glu	Val
	290					295					300				
Thr	Thr	Lys	Met	Leu	Cys	Ala	Ala	Asp	Pro	Gln	Trp	Lys	Thr	Asp	Ser
305					310					315					320
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Ser	Leu	Gln	Gly	Arg
				325					330					335	
Met	Thr	Leu	Thr	Gly	Ile	Val	Ser	Trp	Gly	Arg	Gly	Cys	Ala	Leu	Lys
			340					345					350		
Asp	Lys	Pro	Gly	Val	Tyr	Thr	Arg	Val	Ser	His	Phe	Leu	Pro	Trp	Ile
		355					360					365			
Arg	Ser	His	Thr	Lys	Glu	Gln	Asn	Gly	Leu	Ala	Leu	His	His	His	His
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His	His														
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Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	Phe	Lys	Ile	Ile	Gly
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	50					55					60				
Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	Cys	Gly	Gly	Ser	Leu
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Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys	Phe	Ile	Asp	Tyr
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Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu	Gly	Arg	Ser	Arg	Leu	Asn
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Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	Glu	Asn	Leu	Ile	Leu
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His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	His	Asn	Asp	Ile	Ala
	130					135					140				
Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	Ala	Gln	Pro	Ser	Arg
145					150					155					160
Thr	Ile	Gln	Thr	Ile	Cys	Leu	Pro	Ser	Met	Tyr	Asn	Asp	Pro	Gln	Phe
				165					170					175	
Gly	Thr	Ser	Cys	Glu	Ile	Thr	Gly	Phe	Gly	Lys	Glu	Asn	Ser	Thr	Asp
			180					185					190		
Tyr	Leu	Tyr	Pro	Glu	Gln	Leu	Lys	Met	Thr	Val	Val	Lys	Leu	Ile	Ser
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His	Arg	Glu	Cys	Gln	Gln	Pro	His	Tyr	Tyr	Gly	Ser	Glu	Val	Thr	Thr
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Lys	Met	Leu	Cys	Ala	Ala	Asp	Pro	Gln	Trp	Lys	Thr	Asp	Ser	Cys	Gln

225					230					235				240
Gly	Asp	Ser	Gly	Gly 245	Pro	Leu	Val	Cys	Ser 250	Leu	Gln	Gly	Arg	Met 255
Leu	Thr	Gly	Ile 260	Val	Ser	Trp	Gly	Arg 265	Gly	Cys	Ala	Leu	Lys 270	Asp
Pro	Gly	Val 275	Tyr	Thr	Arg	Val	Ser 280	His	Phe	Leu	Pro	Trp 285	Ile	Arg
His	Thr 290	Lys	Glu	Gln	Asn	Gly 295	Leu	Ala	Leu	Phe	Pro 300	Ile	Pro	Leu
Tyr 305	Cys	Trp	Leu	Cys	Arg 310	Ala	Leu	Ile	Lys	Arg 315	Ile	Gln	Ala	Met
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Pro	Lys	Gly	Ala	Leu 325	Ala	Val	Ala	Val	Ala 330	Gln	Val	Cys	Arg	Val 335
Pro	Leu	Val	Ala 340	Gly	Gly	Ile	Cys	Gln 345	Cys	Leu	Ala	Glu	Arg 350	Tyr
Val	Ile	Leu 355	Leu	Asp	Thr	Leu	Leu 360	Gly	Arg	Met	Leu	Pro 365	Gln	Leu
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Cys	Arg 370	Leu	Val	Leu	Arg	Cys 375	Ser	Met	His	His	His 380	His	His	His